

Amendments to the Specification:

Please replace the paragraph inserted before the first line of the specification as requested on December 6, 2001 with the following amended paragraph:

This application is a Divisional patent application [~~under 37 C.F.R. § 1.53(b)~~] of [~~Continuation~~] U.S. Application No. 09/506,729, now U.S. Patent 6,365,352, filed on February 18, 2000 [~~(pending allowance)~~], which [~~claims priority to~~] is a continuation of PCT International Application No. PCT/US98/17284, filed August 21, 1998, which claims [~~priority to~~] the benefit of U.S. Provisional Application No. 60/056,844, filed on August 22, 1997, all of which are herein incorporated by reference in their entirety.

Please insert the following paragraph before “**Technical Field**” on page 1, line 5 of the specification:

This application is related to application serial No. 08/510,032, serial No. 60/056,844 and application serial No. 08/688,514, all of which are herein incorporated by reference in their entirety. All published articles, patents and other publications cited throughout this application are herein incorporated by reference in their entirety.

Please replace the paragraph beginning on page 9, line 7, with the following amended paragraph:

Figs. 3A and B Figure 3 is an autoradiogram of the expression profile generated from cDNAs made with RNA isolated from neutrophils exposed to avirulent *E. coli* and virulent and avirulent *Y. pestis*. All possible 12 anchoring oligo d(T)_n1, n2 were used to generate a complete expression profile for the enzyme *Bg*III.

Please replace the paragraph beginning on page 13, line 23, with the following amended paragraph:

The oligonucleotide primer that primes first strand DNA synthesis comprises a 5' sequence incapable of hybridizing to a polyA tail of the mRNAs, and a 3' sequence that hybridizes to a portion of the polyA tail of the mRNAs and at least one non-polyA nucleotide immediately upstream of the polyA tail. The 5' sequence is preferably a sufficient length that can serve as a primer for amplification. The 5' sequence also preferably has an average G+C content and does not contain large palindromic sequence; some palindromes, such as a recognition sequence for a restriction enzyme, may be acceptable. Examples of suitable 5' sequences are

CTCTCAAGGATC[~~:]~~TACCGCT (SEQ ID [~~No.~~] NO: 1),

CAGGGTAGACGACGCTACGC (SEQ ID [~~No.~~] NO: 2), and

TAATACCGCGCCACATAGCA (SEQ ID [~~No.~~] NO: 3).

Please replace the paragraph beginning on page 15, line 14, with the following amended paragraph:

The adapters for use in the present invention are designed such that the two strands are only partially complementary and only one of the nucleic acid strands that the adapter is ligated to can be amplified. Thus, the adapter is partially double-stranded (*i.e.*, comprising two partially hybridized nucleic acid strands), wherein portions of the two strands are non-complementary to each other and portions of the two strands are complementary to each other. Conceptually, the adapter is “Y-shaped” or “bubble-shaped.” When the 5' region is non-paired, the 3' end of other strand cannot be extended by a polymerase to make a complementary copy. The ligated adapter can also be blocked at the 3' end to eliminate extension during subsequent amplifications. Blocking groups include dideoxynucleotides or any other agent capable of blocking the 3'-OH. In this type of adapter (“Y-shaped”), the non-complementary portion of the upper strand of the adapters is preferably a length that can serve as a primer for amplification. As noted above, the non-complementary portion of the lower strand need only be one base, however, a longer sequence is preferable (*e.g.*, 3 to 20 bases; 3 to 15 bases; 5 to 15 bases; or 14 to 24 bases). The complementary portion of the adapter should be long enough to form a duplex under conditions of ligation.

Please replace the paragraph beginning on page 23, line 8, with the following amended paragraph:

Synthesis of cDNA was performed as previously described by Prashar *et al.* in WO 97/05286 and in Prashar *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:659-663. Briefly, cDNA was synthesized according to the protocol described in the GIBCO/BRL kit for cDNA synthesis. The reaction mixture for first-strand synthesis included 6 µg of total RNA, and 200 ng of a mixture of 1-base anchored oligo(dT) primers with all three possible anchored bases (ACGTAATACGACTCACTATAGGGCGAATTGGGTCGACTTTTTTTTTTTTTTTTTTn1 wherein n1=A/C or G, SEQ ID NO: 4) along with other components for first-strand synthesis reaction except reverse transcriptase. This mixture was incubated at 65°C for 5m, chilled on ice and the process repeated. Alternatively, the reaction mixture may include 10µg of total RNA, and 2 pmol of 1 of the 2-base anchored oligo(dT) primers a heel such as RP5.0 (CTCTCAAGGATCTTACCGCTT₁₈AT, SEQ ID NO: 5), or RP6.0 (TAATACCGCGCCACATAGCAT₁₈CG, SEQ ID NO: 6), or RP9.2 (CAGGGTAGACGACGCTACGCT₁₈GA, SEQ ID NO: 7) along with other components for first-strand synthesis reaction except reverse transcriptase. This mixture was then layered with mineral oil and incubated at 65°C for 7 min followed by 50°C for another 7 min. At this stage, 2µl of Superscript reverse transcriptase (200 units/µl; GIBCO/BRL) was added quickly and mixed, and the reaction continued for 1 hr at 45-50°C. Second-strand synthesis was performed at 16°C for 2 hr. At the end of the reaction, the cDNAs were precipitated with ethanol and the yield of cDNA was calculated. In our experiments, ≈200 ng of cDNA was obtained from 10µg of total RNA.

Please replace the paragraph beginning on page 24, line 1, with the following amended paragraph:

The adapter oligonucleotide sequences were A1 (TAGCGTCCGGCGCAGCGACGGCCAG, SEQ ID NO: 8) and A2 (GATCCTGGCCGTCGGCTGTCTGTCGGCGC, SEQ ID NO: 9). One microgram of oligonucleotide A2 was first phosphorylated at the 5' end using T4 polynucleotide kinase (PNK). After phosphorylation, PNK was heated denatured, and 1µg of the oligonucleotide A1 was

added along with 10× annealing buffer (1 M NaCl/100 mM Tris-HCl, pH8.0/10 mM EDTA, pH8.0) in a final vol of 20 µl. This mixture was then heated at 65°C for 10 min followed by slow cooling to room temperature for 30 min, resulting in formation of the Y adapter at a final concentration of 100 ng/µl. About 20 ng of the cDNA was digested with 4 units of *Bgl* II in a final vol of 10 µl for 30 min at 37°C. Two microliters (≈4 ng of digested cDNA) of this reaction mixture was then used for ligation to 100 ng (≈50-fold) of the Y-shaped adapter in a final vol of 5µl for 16 hr at 15°C. After ligation, the reaction mixture was diluted with water to a final vol of 80 µl (adapter ligated cDNA concentration, ≈50 pg/µl) and heated at 65°C for 10 min to denature T4 DNA ligase, and 2-µl aliquots (with ≈100 pg of cDNA) were used for PCR.

Please replace the paragraph beginning on page 24, line 17, with the following amended paragraph:

The following sets of primers were used for PCR amplification of the adapter ligated 3' -end cDNAs:

TGAAGCCGAGACGTCGGTCG(T)₁₈ n1, n2 (wherein n1, n2 = AA, AC, AG AT CA CC CG CT GA GC GG and GT; SEQ ID NO: 10) as the 3' primer with A1 as the 5' primer or alternatively

RP 5.0, RP 6.0, or RP 9.2 used as 3' primers with primer A1.1 serving as the 5' primer. To detect the PCR products on the display gel, 24 pmol of oligonucleotide A1 or A1.1 was 5' -end-labeled using 15 µl of [γ -³² P]ATP (Amersham; 3000 Ci/mmol) and PNK in a final volume of 20 µl for 30 min at 37°C. After heat denaturing PNK at 65°C for 20 min, the labeled oligonucleotide was diluted to a final concentration of 2 µM in 80 µl with unlabeled oligonucleotide A1.1. The PCR mixture (20µl) consisted of 2 µl (≈100 pg) of the template, 2µl of 10× PCR buffer (100 mM Tris-HCl, pH 8.3/500 mM KCl), 2 µl of 15 mM MgCl₂ to yield 1.5 mM final Mg²⁺ concentration optimum in the reaction mixture, 200 µM dNTPs, 200 nM each 5' and 3' PCR primers, and 1 unit of Amplitaq Gold. Primers and dNTPs were added after preheating the reaction mixture containing the rest of the components at 85°C. This "hot start" PCR was done to avoid ~~artefactual~~ artifactual amplification arising out of arbitrary annealing of PCR primers at lower temperature during transition from room temperature to 94°C in the first PCR cycle. PCR consisted of 5 cycles of 94°C for 30 sec, 55°C for 2 min, and 72°C for 60 sec followed by 25

cycles of 94°C for 30 sec, 60°C for 2 min, and 72°C for 60 sec. A higher number of cycles resulted in smeary gel patterns. PCR products (2.5µl) were analyzed on 6% polyacrylamide sequencing gel. For double or multiple digestion following adapter ligation, 13.2 µl of the ligated cDNA sample was digested with a secondary restriction enzyme(s) in a final vol of 20 µl. From this solution, 3µl was used as template for PCR. This template vol of 3 µl carried ≈ 100 pg of the cDNA and 10 mM MgCl₂ (from the 10× enzyme buffer), which diluted to the optimum of 1.5 mM in the final PCR vol of 20 µl. Since Mg²⁺ comes from the restriction enzyme buffer, it was not included in the reaction mixture when amplifying secondarily cut cDNA. Bands were extracted from the display gels as described by Liang *et al.* (1995 *Curr. Opin. Immunol.* 7:274-280), reamplified using the 5' and 3' primers, and subcloned into pCR-Script with high efficiency using the PCR-Script cloning kit from Stratagene. Plasmids were sequenced by cycle sequencing on an ABI automated sequencer.

Please replace Table 2, beginning on page 37 with the following Table 2.

TABLE 2

Cln	Sequence
846	<p>1 TCTCAGTGAG CTGAGATCAC ACCACTGCAC TCCAAGTGGG CGACAGAGCA</p> <p>51 AG (<u>SEQ ID NO: 11</u>)</p>
854	<p>1 CACTTCCCC AAATTCTTTT GCCATAGTTC ACTCTCTACT GATAAGGCCA</p> <p>51 C. (<u>SEQ ID NO: 12</u>)</p>

855	<p>1 GGGAAAGTGG TGGGGTGGTG AGGGTCAATG TGCAGAAAAT CGATGTAACT</p> <p>51 TGTAATACAG TTGAGTCAAC TGTGTGTTCA CAACAACTCT GAGAGTTAAC</p> <p>101 ACCATTTCTA C (<u>SEQ ID NO: 13</u>)</p>
856	<p>1 ATCTAAATAT TTTTCATACC GAGTTATTAA GGAGTCAGTA GTCTGTGCTA</p> <p>51 CAATGCTGCA AAAAGCATCA CGTGGAAGAA TGGGAACTAT GCGTACTTTA</p> <p>101 TGAAGTGATG TATAACACAA TGAAGTCTGT TTTACAAC TA CAGTGCTGCA</p> <p>151 TTCAATTATC TTCCAT (<u>SEQ ID NO: 14</u>)</p>
859	<p>1 AAGCTCTGTA TACAAAAGTT ATTTATTTAG ATGTTGAGG CATGTCTCTC</p> <p>51 CTCACCTGTA AACTAACTGT TTTATAACAG CTTGTATCAC ATGTGTGAAG</p> <p>101 TTAATGAATG TAATACTCCA ACAAGCCATT CATCAGATTG GCCAACAGCT</p> <p>151 AGGATACAGT TAAATAATGG CGACCAGGTT GACAAGTCAT AATTGCGGTT</p> <p>201 TGGGGGACCG TAGTTGCACC TCACCTAGAC CAACGTACGC ATGGCACTCG</p> <p>251 ACCCAGGCGA ACAAATTA T (<u>SEQ ID NO: 15</u>)</p>

863

1 TTTCTCAAGA AGAGATAAGA ATGAAAAGTC ATAGAACACA
TCATGGAGGA

51 CCTGGACACA AATGCAGACA AGCAGCTGAG CTTCGAGGAG
TTCATCATGC

101 TGATGGCGAG GCTAACCTGG GCCTCCCACG AGAAGATGCA
CGAGGGTGAC

151 GATGGCCCTG GCCACCACCA TAAGCCAGGC CTCGGGGAGG
GCACCCCCTA

201 AGACCACAGT GGACAAGATC ACAGTGGCCA CGGACACGGC
CACAGTCATG

251 GTGGCCACGG CCACAGCCAC TAATCAGGAG GCCAGGCCAC
CCTGCCTCTA

301 CCCAACCAGG GCCCCGGGGC CTGTTATGTC AAAGTGTCTT
GGCTGTGGGG (SEQ ID NO: 16)

866	<p>1 NGATCTTTCT AGGAGGGAGA CACTGGCCNC TCAAATCGTC CAGCGACCTT</p> <p>51 CCTCATCCAC CCCATCCCTC CCCAGTTCAT TGCACTTTGA TTAGCAGCGG</p> <p>101 AACAAGGAGT CAGACATTTT AAGATGGTGG CAGTAGAGGC TATGGACAGG</p> <p>151 GCATGCCACG TGGGCTCATA TGGGGCTGGG AGTAGTTGTC TTTCCTGGCA</p> <p>201 CTAACGTTGA GCCCCTGGAG GCACTGAAGT GCTTAGTGTA CTTGGAGTAT</p> <p>251 TGGGGTCTGA CCCCAAACAC CTTCCAGCTC CTGTAACATA CTGGCCTGGA</p> <p>301 CTGTTTTCTC TCGGCTCCCC ATGTGTCCTG GTTCCCGTTT CTCCACCTAG</p> <p>351 ACTGTGAACC TCTCGAGGGC AGGGACCACA CCCTGTACTG TTCTGTGTCT</p> <p>401 TTCACAGCTC CTCCCACAAT GCTGAATATA CAGCAGGTGC TCAATAAATG</p> <p>451 ATTCT (<u>SEQ ID NO: 17</u>)</p>
871	<p>1 GCAAGTGTGT TGTGTTACAG TGTCACAACA CCGAG (<u>SEQ ID NO: 18</u>)</p>
872	<p>1 GATCTCTCCC TACGCAAAAC GTATTGTAGT GAAAGGGTCT TCTTTACTAC</p> <p>51 CTTAATAAAA CAGCTAGTGT G (<u>SEQ ID NO: 19</u>)</p>

874	1 GATCTAAATA CAAAGGATAT ACAGTCTTGA ATCTAAAATA ATTTGCTAAC 51 TATTTTGATT CTTCAGAGAG AACTACTA (SEQ ID NO: 20)
876	1 GATCTAGTCC GGACATGCTG TGTATATTGT AACGTAAAT GAAAAAAGAA 51 CCCCCCTTTG TATTATAGTC ATGCGGTCTT ATGTATGATA AACAGTTG (SEQ ID NO: 21)
878	1 GATCTTTTGT AGTCACCTCT GTATCTTATG TCTGGTTGAG GGGTGCTTTT 51 ACTTGTCTGG CATTTGCATT CAATGATCTT TCAGTCATGT CAGTTAGACT 101 AAAAATTATT TCTG (SEQ ID NO: 22)
880	1 CCCAAGCCCC TTGGACACTG CAGCTCTTTT CAGTTTTTGC TTACACACAA 51 TTCATTCTTT GCAGCTAATT AAGCCGAAGA AGCGTGGGAA TCAAGTTTGG 101 AACAGAGATT AAAAAAGTTC TT (SEQ ID NO: 23)
881	1 GCTCTGGAGG ACAATCCAGG AACTACATTA CCTGGACTGT ATGCTGGTCA 51 TTTCTACAGA CAGCATTCAG TATTTGAGTG TACGGTAACT GTCTGGGGTG 101 ATTCCTATAA GATCATTATA CTG (SEQ ID NO: 24)

882	<p>1 GATCTTTCTC CTTGAATATC TTTCGATAAA CAACAAGGTG GTGTGATCTT</p> <p>51 AATATATTTG AAAAAAACTT CATTCTCGTG AGTCATTAA ATGTGTACAA</p> <p>101 TGTACACACT GGTACTTAGA GTTTCTGTTT GATTCTTTTT TAATAAACTA</p> <p>151 C (<u>SEQ ID NO: 25</u>)</p>
883	<p>1 TGTCATCAT GCCCTGGGAC TGCTTCTCCA GCCAGGCGGG CGCCATACGT</p> <p>51 CCCACACTAG TGAAGGTCAA TGTCTCAGAA CAACACCTCT AT (<u>SEQ ID NO: 26</u>)</p>
884	<p>1 GATCTGGCCT GTTCCTGCGT CTGCGGAGCA GGCCTTGTCT CCCAGCTATC</p> <p>51 TATAACCTTA CCTAGAGTGT CGACTTGTGG GTTCCTGTTG CTGAGACTTC</p> <p>101 CTGGATGGAG CCGCCCTCAC CGCCGGACCC GTAGCACTGC GCGGAACTGT</p> <p>151 GTCCAATAAA GT (<u>SEQ ID NO: 27</u>)</p>
885	<p>1 GATCTGATTT GCTAGTTCTT CCTTGTAGAG TTATAAATGG AAAGATTACA</p> <p>51 CTATCTGATT AATAGTTTCT TCATACTCTG CATATAATTT GTGGCTGCAG</p> <p>101 AATATTGTAA TTTGTTGCAC ACTATGTAAC AAAACAACCTG AAGATATGTT</p> <p>151 TAATAAATAT TGTACT (<u>SEQ ID NO: 28</u>)</p>

894	<p>1 GATCTTTATG AGAGCAGTAT TTTCTGTGTT TTCTTTTAA TTTACAGCCT</p> <p>51 TTCTTATTTT GATATTTTTT TAATGTTGTG GATGAATGCC AGCTTTCAGA</p> <p>101 CAGAGCCAC TTAGCTTGTC CACATGGATC TCAATGCCAA TCCTCCATTC</p> <p>151 TTCCTCTCCA GATATTTTTG GGAGTGACAA ACATTCTCTC ATCCTACTTA</p> <p>201 GCCTACCTAG ATTTCTCATG ACGAGTTAAT GCATGTCCGT GGTTGGGTGC</p> <p>251 ACCTGTAGTT CTGTTTATTG GTCA (<u>SEQ ID NO: 29</u>)</p>
895	<p>1 GATCTAAGTT AGTCCAAAAG CTAAATGATT TAAAGTCAAG TTGTAATGCT</p> <p>51 AGGCATAAGC ACTCTATAAT ACATTAAATT ATAGGCCGAG CAATTAGGGA</p> <p>101 ATGTTTCTGA AACATTAAAC TTGTATTTAT GTCACTAAAA TTCTAACACA</p> <p>151 AACTTAAAAA ATGTGTCTCA TACATATGCT GTACTAGGCT TCATCATGCA</p> <p>201 TTTCTAAATT TGTGTATGAT TTGAATATAT GAAAGAATTT ATACACGAGT</p> <p>251 GTTATTTAAA ATTATTAAAA ATAAATGTA (<u>SEQ ID NO: 30</u>)</p>

896	<p>1 GATCTTATAG GCCTGTCTCA TCAGGTTGGT GTCAGCCCAG CTAGGATTAG</p> <p>51 GCAGAATTGG GTGGGGGCTG TAGTGCACTT TTGGCACAGC ATGTACCTGT</p> <p>101 CTGACTAATT CTCTGTCTTT TCTTTCCTGT TGCAATTCAT GGGTCTTAGC</p> <p>151 ATCTTCTGAA TGGTGTTTAG TAGGTCATCC TGTTGATTTC CTGCTAGGGA</p> <p>201 GTAGCATACT CTGGCTCTGT ACCACTGGCC AAGGGACTTA AGGATAGATG</p> <p>251 AAGGGCTGCA GTTTTGTAA ATGGAACAAT ATGAAGAGA (<u>SEQ ID NO: 31</u>)</p>
T10 3	<p>1 GATCTTTCTC CTTGAGTATC TTTCGATAAA CAACAAAGTG GTGTGATCTT</p> <p>51 AATATATTTG AAAAAAACTT CATTCTCGTG AGTCATTAA ATGTGTACAA</p> <p>101 TGTACACACT GGTACTTAGA GTTCTGTTT GATTCTTTTT TAATAAACTA</p> <p>151 C (<u>SEQ ID NO: 32</u>)</p>
T10 4	<p>1 GATCTCTGCT CATAGAATGC ATGGGGAGCC TTCCAGCTCA CTCTCCCTGA</p> <p>51 GGACTGGCTT GACAGGGGCT ATGGGTTTGC TTTGG (<u>SEQ ID NO: 33</u>)</p>

<p>T10 5</p>	<p>1 GATCTGCGCT TCCAGAGCGC AGCTATCGGT GCTTTGCAGG AGGCAAGTGA</p> <p>51 GGCCTATCTG GTTGGCCTTT TTGAAGACAC CAACCTGTGT GCTATCCATG</p> <p>101 CCAAACGTGT AACAATTATG CCAAAAGACA TCCAGCTAGC ACGCCGCATA</p> <p>151 CGTGGAGAAC GTGCTTAAGA ATCCACTATG ATGGGAAACA (<u>SEQ ID NO: 34</u>)</p>
<p>T10 7</p>	<p>1 GATCTAAATG TGAACAGTTT ACTAATGCAC TACTGAAGTT TAAATCTGTG</p> <p>51 GCACAATCAA TGTAAGCATG GGGTTTGTTT CTCTAAATTG ATTTGTAATC</p> <p>101 TGAAATTACT GAACAACCTCC TATTCCCATT TTTGCTAAAC TCAATTTCTG</p> <p>151 GTTTTGGTAT ATATCCATTC CAGCTTAATG CCTCTAATTT TAATGCCAAC</p> <p>201 AAAATTGGTT GTAATCAAAT TTAAAAATAA TAATAATTTG GC (<u>SEQ ID NO: 35</u>)</p>
<p>T76</p>	<p>1 GCCTTTTCGA TAGTTTCGGG TCAGGTAAAA ATGGCCTCCT GGC GTAAGCT</p> <p>51 TTTCAAGGTT TTTTGGAGGC TTTTGTAAA TTGTGATAGG AACTTTGGAC</p> <p>101 CTTGAACTTA CGTATCATGT GGAGAAGAGC CAATTTAACA AACTAGGAAG</p> <p>151 ATGAAAAGGG AAATTGTGGC CAAAACCTTG GGAAAAGGAG GTTCTTAAAA</p> <p>201 TCAGTGTTTC CCCTTT (<u>SEQ ID NO: 36</u>)</p>

T8	<p>1 GATCTATGCA CAAGAACCCC TTTACCCCAT GACCAACATC GCAGACACAT</p> <p>51 GTGCTGGCCA CCTGCTGAGC CCCAAGTGGG ACGAGACAAG CAGCCCTTAG</p> <p>101 CCCTTCCCCT CTGCAGCTTC CAGGCTGGCG TGCAGCATCA GCATCCCTAG</p> <p>151 AAAGCCATGT GCAGCCACCA GTCCATTGGG CAGGCAGATG TTCCTAATAA</p> <p>201 AGCT (<u>SEQ ID NO: 37</u>)</p>
T81	<p>1 GATCTTTCCT CCTGGTTACT GTGAAGCCTG TTGGTTTGCT GCTGTCGTTT</p> <p>51 TTGAGGAGGG CCCATGGGGG TAGGAGCAGT TGAACCTGGG AACAAACCTC</p> <p>101 ACTTGAGCTG TGCCTAGACA ATGTGAATTC CTGTGTTGCT AACAGAAGTG</p> <p>151 GCCTGTAAGC TCCTGTGCTC CGGAGGGAAG CATTTCTGG TAGGCTTTGA</p> <p>201 TTTTCTGTG TGTAAAGAA ATTCAATCTA CTCATGATGT GTTATGCATA</p> <p>251 AAACATTTCT GGAACATGGA TTTGTGTCA CCTTAAATGT GAAAATAAAT</p> <p>301 CCTA (<u>SEQ ID NO: 38</u>)</p>

T82	<p>1 ATCTTTCCTC CTGGTTACTG TGAAGCCTGT TGGTTTGCTG CTGTCGTTTT</p> <p>51 TGAGGAGGGC CCATGGGGGT AGGAGCAGTT GAACCTGGGA ACAAACCTCA</p> <p>101 CTTGAGCTGT GCCTAGACAA TGTGAATTCC TGTGTTGCTA ACAGAAGTGG</p> <p>151 CCTGTAAGCT CCTGTGCTCC GGAGGGAAGC ATTCCTGGT AGGCTTTGAT</p> <p>201 TTTTCTGTGT GTTAAAGAAA TTCAATCTAC TCATGATGTG TTATGCATAA</p> <p>251 AACATTTCTG GAACATGGAT TTGTGTTTAC CTAAATGTG AAAATAAATC</p> <p>301 CTATTTTCTA TG (SEQ ID NO: 39)</p>
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T85	<p>1 GATCTTTGGC AGCGCCATTG GACTCTTTGG GGTATCGTC GCAATTCTTC</p> <p>51 ATACCTCCAG AGTGAAGATG GGTGACTAGA TGATATGTGT GGGTGGGGCC</p> <p>101 GTGCCTCACT TTTATTTATT GCTGGTTTTTC CTGGGACAGC TGGAGCTGTG</p> <p>151 TCCCTTAACC TTTCAGAGGC TTGGTGTTCA GGGCCCTCCC TGCACTCCCC</p> <p>201 TCTTGCTGCG TGTTGATTTG GAGGCACTGC AGTCCAGGCC GAGTCCTCAG</p> <p>251 TCGGGGAGC AGGCTGCTGC TGCTGACTCT GTGCAGCTGC GCACCTGTGT</p> <p>301 CCCCCACCTC CACCCTCAAC CCATCTTCCT AGTGTTTG TG AAATAAACTT</p> <p>351 GGTAT (SEQ ID NO: 40)</p>
T98	<p>1 GATCTTCCAC GTCTCCATCT CAGTACACAA TCATTTAATA TTTCCCTGTC</p> <p>51 TTACCCCTAT TCAAGCAACT AGAGGCCAGA AAATGGGCAA ATTATCACTA</p> <p>101 ACAGGTCTTT GACTCAGGTT CCAGTAGTTC ATTCTAATGC CTAGATTCTT</p> <p>151 TTGTGGTTGT TGCTGGCCCA ATGAGTCCCT AGTCACATCC CCTGCCAGAG</p> <p>201 GGAGTTCTTC TTTTGTGAGA GACACTGTAA ACGACACAAG AGAACAAGAA</p> <p>251 TAAAA (SEQ ID NO: 41)</p>

933	1 TTATATATTT TTCTTAAATA TGTTTTATTG TCTTCTCTAA GCAAAAAGTT
	51 CTTAATAAAC ATAGTATTTT TCTCTGCGTC CTATTTCAATT AGTGAAGACA
	101 TAGTTCACCT AAAATGGCAT CCTGCTCTGA ATCTAGACTT TTTAGAAATG
	151 GCATATGTTT TTGATGATAT GTCAACATTC AAAATAGTCC TAATTAAATT
	201 GTTGGTTAAA TGTAATGTCA ACTCTTTATA AACTTAAATA TAAACAAGTA
	251 ATTAACCACT CTAAGTAATA AAACACATTT CACCTGTGTT CTGAGTGTA (SEQ ID NO: 42)

967

1 ATGAATCCTT GCCACCTCCA CCTGCAGAAC TGTATAAAT ATTACAACCTT
51 GCTTTTTAGC TGATCTTCCA TCCTCAAATG ACTCTTTTTT CTTTATATGT
101 TAACATATAT AAAATGGCAA CTGATAGTCA ATTTTGATT
TTATTCAGGA
151 ACTATCTGAA ATCTGCTCAG AGCCTATGTG CATAGATGAA ACTTTTTTTTT
201 AAAAAAAGTT ATTTAACAGT AATCTATTTA CTAATTATAG TACCTATCTT
251 TAAAGTATAG TACATTTTAC ATATGTAAAT GGTATGTTTC AATAATTAA
301 GAACTCTGAA ACAATCTACA TATACTTATT ACCCAGTACA GTTTTTTTTC
351 CCCTGAAAAG CTGTGTATAA AATTATGGTG AATAAACTTT
TATGTTTCCA
401 TTTCAAAGAC CAGGGTGGAG AGGAATAAGA GACTAAGTAT
ATGCTTCAAG
451 TTTTAAATTA ATACCTCAGG TATTAAAATA AATATTCCAA
GTTTGTGGGA
501 AATGGGGAGA TTAAAATG (SEQ ID NO: 43)

978	1 TTATGTGGCC TTAGGTAGCT GGTTGTACAT CTTCCCTAA ATCGATCCAT
	51 GTTACCACAT AGTAGTTTTA GTTTAGGATT CAGTAACAGT GAAGTGTTTA
	101 CTATGTGCAA CGGTATTGAA GTTCTTATGA CCACAGATCA TCAGTACTGT
	151 TGTCTCATGT AATGCTAAAA CTGAAATGGT CCGTGTTTGC ATTGTTAAAA
	201 ATGATGTGTG AAATAGAATG AGTGCTATGG TGTTGAAAAC TGCAGTGTCC
	251 GTTATGAGTG CCAAAAATCT GTCTTGAAGG CAGCTACACT TTGAAGTGGT
	301 CTTGAATAC TTTTAATAAA TTTATTTTGA TA <u>(SEQ ID NO: 44)</u>

981

1 TAGGTGAACC CTTATTCTGC AGGGTTCTCC CTCCCACCTT AAAGAAGTTC

51 CCCTTATGTG GGTTCCTGG TGAATGGCCT TCCTTCCCGC CAGAGGGCTT

101 GTGAACAGAC CGGAGAGGAC AGTGGATTGT TTATACTCCA
GTGTACATAG

151 TGTAATGTAG CGTGTTTACA TGTGTAGCCT ATGTTGTGGT CCATCAGCCC

201 CTCACATTCC TAGGGGTTTG AGATGCTGTA CGTGGTATGT
GACACCAAAG

251 CCACCTCTGT CATTGTGTGT GATGTCCTTT CTTGGCAAAA GCCTTGTGTA

301 TATTTGTATA TTACACATTT GTACAGAATT TTGGAAGATT TTCAGTCTAG

351 TTGCCAAATC TGGCTCCTTT ACAAAG (SEQ ID NO: 45)

982	<p>1 AGAATCTCTT ATGTTCTCAG AGGAAGGTGG AAGAAACCAT GGGCAGGAGT</p> <p>51 AGGAATTGAG TGATAAACAA TTGGGCTAAT GAAGAAAAC TCTCTTATTG</p> <p>101 TTCAGTTCAT CCAGATTATA ACTTCAATGG GACACTTTAG ACCATTAGAC</p> <p>151 AATTGACACT GGATTAAACA AATTCACATA ATGCCAAATA CACAATGTAT</p> <p>201 TTATAGCAAC GTATAATTTG CAAAGATGGA CTTTAAAAGA TGCTGTGTAA</p> <p>251 CTAAACTGAA ATAATTCAAT TACTTATTAT TTAGAATGTT AAAGCTTATG</p> <p>301 ATAGTCTTTT CTAATTCTTA AACTCATACT TTGAAATCTT TCTGAGTTTC</p> <p>351 CCCAGAAGAG AATATGGGAT TTTTTTTGAC ATTTTGTACT CATTTAATAA</p> <p>401 TGCTCTTGTG TTTACCTAGT ATATGTAGAC TTTGTCTTAT GTGTCAAAAG</p> <p>451 TCCTAGGAAA GTGGTTGATG TTTCTTATAG CAATTAAAAA TTATT (SEQ ID NO: 46)</p>
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905	<p>1 ATCTCAGTGA GCTGAGATCA CACCACTGCA CTCCAACCTGG GCGACAGAGC</p> <p>51 AAGA (SEQ ID NO: 47)</p>
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910	<p>1 GATCTGTAAT TCAGGTGTTT TCTGTACAGC CATACTAGA TAATGAAGCC</p> <p>51 AAAAGGCTTT TAATTACACC ATGGCCTAAA ATAAATTCAT CA (<u>SEQ ID NO: 48</u>)</p>
915	<p>1 TATTTTTCAG CTGAGTTATT AGGGAGTCAT TATTCTGTGG TACAATGCTG</p> <p>51 CAAAAAGCAT CATGTGGAAG AATGGGAACT ATGCTTACAT TATGAAGTGA</p> <p>101 TGTATAACAC AATGCAAATC TG (<u>SEQ ID NO: 49</u>)</p>
916	<p>1 GATCTTTTTT CATTAAAAAA TGTTCATTA TCAGGCCGGG TGCAGTGGGG</p> <p>51 CTCATGCCTG TAATCCCAAC ACTTTGGGAG GCCGATGCAG GCGGATCACT</p> <p>101 AGGTCAGCAG ATCGAGACCA TCCTGGCTAA CACAGTGAAA CCT (<u>SEQ ID NO: 50</u>)</p>
921	<p>1 GATCTTTATT TTAGCCATG CACTGTTGTG AGGAAAATTA CCTGTCTTGA</p> <p>51 CTGCCATGTG TTCATCATCT TAAGTATTGT AAGCTGCTAT GTATGGATTT</p> <p>101 AAACCGTAAT CATATCTTTT TCCTATCTAT CTGAGGCACT GGTGGAATAA</p> <p>151 AGAACCTGTA TATTTTACTT TGTGTCAGAT AGTCTTGCCG CATCTTGGCA</p> <p>201 AGTTGCAGAG A (<u>SEQ ID NO: 51</u>)</p>

927	<p>1 GATCTTCGTG AAGACCTGAC TGGTAAGACC ATCACCTCG AGGTGGAGCC</p> <p>51 CAGTGACACC ATCGAGAATG TCAAGGCAAA GATCCAAGAT AAGGAAGGCA</p> <p>101 TCCCTCCTGA TCAGCAGAGG TTGATCTTTG CTGGGAAACA GCTGGAAGAT</p> <p>151 GGACGCACCC TGTCTGACTA CAACATCCAG AAAGAGTCCA CTCTGCACTT</p> <p>201 GGTCTGCGC TTGAGGGGGG GTGTCTAAGT TTCCCCTTTT AAGGTTTCAA</p> <p>251 CAAATTTTCAT TGCACCTTCC TTTCAATAAA GTTG <u>(SEQ ID NO: 52)</u></p>
928	<p>1 GATCTTTCCT CCTGGTTACT GTGAAGCCTG TTGGTTTGCT GCTGTCGTTT</p> <p>51 TTGAGGAGGG CCCATGGGGG TAGGAGCAGT TGAACCTGGG AACAAACCTC</p> <p>101 ACTTGAGCTG TGCCTAGACA ATGTGAATTC CTGTGTTGCT AACAGAAGTG</p> <p>151 GCCTGTAAGC TCCTGTGCTC CGGAGGGAAG CATTCCTGG TAGGCTTTGA</p> <p>201 TTTTCTGTG TGTAAAGAA ATTCAATCTA CTCATGATGT GTTATGCATA</p> <p>251 AAACATTTCT GGAACATGGA TTTGTGTTCA CCTTAAATGT GAAAATAAAT <u>(SEQ ID NO: 53)</u></p>

930	<p>1 GATCTTTCGG GTTCTCTCTC CTAACCTCAGC TCTTCGTTCC CAGAAACCCA</p> <p>51 GATGTAATCC CCCTACGTGG TGCTTGGGGC ATCCCGATAC CATCTCAGTA</p> <p>101 AATCTCCTAC ATTGGCCTCC TCACCCTCCC CGGGACCCAC ACCCTTCAGG</p> <p>151 TCCTCACCT GAGACAGGAG GGACCCTCTG AGATCAGGGA CCCTTAGGTC</p> <p>201 TCACTGCTCT CTGATTCATA GCTCAACTGG GCCCCAGTT CCATACCCCA</p> <p>251 GCATTCCCGG TCACTCCCTC CCTAATCTGA GCATCACTCA AGCTCTTTAT</p> <p>301 TAAACTC (<u>SEQ ID NO: 54</u>)</p>
939	<p>1 ATCTCTCTCC CTACGCAAAA CCCTATTGTA GTAAAAAAGT CTTCTTTACT</p> <p>51 ATCTTAATAA AACAGATATT GTG (<u>SEQ ID NO: 55</u>)</p>
945	<p>1 ATCTATTCTT GTAGATTTTT TTTGTGTGGG TCTATGTTTC ATTCATCTGC</p> <p>51 TTTCAGGCTG GATTTATAAC AAGCAGAACT TTAAAACG (<u>SEQ ID NO: 56</u>)</p>
949	<p>1 GATCTAAATA TTTTTCAGCT GAGTTATTAC GGAGTCATTA TTCTGTGGTA</p> <p>51 CAATGCTGCA AAAAGCATCA TGTGGAAGAA TGGGAACTAT GCTTACTTTA</p> <p>101 TGAAGTGATG TATAACACAA TGAAA (<u>SEQ ID NO: 57</u>)</p>

952	<p>1 CTACCCCGTG ACTCAGTTAC CTCCCCTGG GTCCCTCCCA CATCATGTGG</p> <p>51 GAATTGTAGG AGCTACAATT CAAGATGAGA TTTGGATGGG GTCACAGCCA</p> <p>101 AACCATATCA CTGAGGTATC AAGGAGATTC TT <u>(SEQ ID NO: 58)</u></p>
954	<p>1 GATCTGATTT GCTAGTTCTT CCTGTAGAG TTATAAATGG AAAGATTACA</p> <p>51 CTATCTGATT AATAGTTTCT TCATACTCTG CATATAATTT GTGGCTGCAG</p> <p>101 AATATTGTAA TTTGTTGCAC ACTATGTAAC AAAACAAC TG AAGATATGTT</p> <p>151 TAATAAATAT TGTACTTATT G <u>(SEQ ID NO: 59)</u></p>
975	<p>1 NGATCTTTCT CCTTGAATAT CTTTCGATAA ACAACAAGGT GGTGTGATCT</p> <p>51 TAATATATTT GAAAAAACT TCATTCTCGT GAGTCATTTA AATGTGTACA</p> <p>101 ATGTACACAC TGGTACTTAG AGTTTCTGTT TGATTCTTTT TTAATAAA <u>(SEQ ID NO: 60)</u></p>

976	<p>1 GATCTGCTAG AAGATGGTTT TGGAGAGCAC CCCTTTTACC ACTGCCTGGT</p> <p>51 TGCAGAAGTG CCGAAAGAGC ACTGGACTCC GGAAGGTAAC CCCTCGCCCT</p> <p>101 TTCCAGAAGC CAGAGAGACC AAGTGTTATG TAAGAAGTAG TGTCGGCTGT</p> <p>151 GTAGAACCAC TGA CTACACA GGCCGAAGTT ACTGAGAACT TGGACAGAAA</p> <p>201 AAATAGCCAG CAAGTGTT (<u>SEQ ID NO: 61</u>)</p>
984	<p>1 CATTACACA TTAACTCC TTCCATACCA AATCTT (<u>SEQ ID NO: 62</u>)</p>
986	<p>1 GATCTGGACA GCAGAATGTT ATAACGCAAG TTCATGTGTT GCTCCCAACT</p> <p>51 CCATTCTCTT TTCTCTCGTG CAACCAGTTT GCCATTCTC TTCCTATTAC</p> <p>101 TTGCTC (<u>SEQ ID NO: 63</u>)</p>
T11 3	<p>1 TCAGAGATTT GCAAAGACTC ACGTTTTTGT TGTTTTCTCA TCATTCCATT</p> <p>51 GTGATACTAA GAACTAAGA AGCTTAATGA AAAGAAATAA AATGCCTATG (<u>SEQ ID NO: 64</u>)</p>

<p>T11 6</p>	<p>1 GATCTGCGCT TCCAGAGCGC AGCTATCGGT GCTTTGCAGG AGGCAAGTGA</p> <p>51 GGCCTATCTG GTTGGCCTTT TTGAAGACAC CAACCTGTGT GCTATCCATG</p> <p>101 CCAAACGTGT AACAATTATG CCAAAAGACA TCCAGCTAGC ACGCCGCATA</p> <p>151 CGTGGAGAAC GTGCTTAAGA ATCCACTATG ATGGGAAACA (<u>SEQ ID NO: 65</u>)</p>
<p>T12 3</p>	<p>1 GATCTGTGAA ATGCTATCTC TCCTGAAGCA ATACTGTTGA CCAGAAAGGA</p> <p>51 CACTCCATAT TGTGAAACCG GCCTAATTTT TCTGACTGAT ATGGAAACGA</p> <p>101 TTGCCAACAC ATACTTCTAC TTTTAAATAA ACAACTTTGA TGATGTAAC</p> <p>151 TGACCTTCCA GAGTTATGGA AATTTTGTCC CCATGTAATG AATAAATTGT</p> <p>201 ATGTAT (<u>SEQ ID NO: 66</u>)</p>